IN THE SPECIFICATION:

Please delete the Sequence Listing of record and insert the substitute Sequence Listing provided herewith in the above-identified application.

REMARKS

In response to the Office Communication dated September 26, 2001 and in accordance with the provisions in 37 C.F.R. §1.821-§1.825, Applicants submit herewith a substitute paper and an initial computer readable copy of the Sequence Listing, along with a Statement Under 37 C.F.R. §1.821(f), stating that these copies are identical. A copy of the Notice to Comply is also enclosed.

The substitute Sequence Listing is compiled using Patent In Version 2.1. Applicants have also corrected certain typographical errors in the original Sequence Listing. More specifically, Applicants have made corrections in the section of total length in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 6 and SEQ ID NO: 7 to reflect the correct length of these molecules. In addition, Applicants have corrected a typographical error in the sequence of SEQ ID NO: 7 at nucleotide number 505-507: the codon "TGA" has been replaced with "TCA". It is respectfully submitted that those skilled in the art would have readily recognized the stop codon "TGA" in the original Sequence Listing of SEQ ID NO: 7 to be an obvious typographical error. As described in the specification at page 8, lines 7-24, SEQ ID NO: 7 is a derivative of the murine *bcl-w* sequence as set forth in SEQ ID NO: 3. Thus, those skilled in the art would have looked to SEQ ID NO: 3 (murine *bcl-w*) and would have recognized that the codon TGA should

read "TCA" instead. Similarly, the symbol "*" (representing stop codon encoded by TGA) in SEQ ID NO: 8 should read "Ser" (encoded by the codon TCA).

It is respectfully submitted that the above amendment to the Sequence Listing does not introduce new matter. A marked-up version of the Sequence Listing is enclosed to show the changes made. Applicants have also amended the specification to insert the substitute Sequence Listing.

In view of the foregoing Amendment and the Remarks, it is believed that the subject case is in condition for an examination on the merits, which action is earnestly solicited.

Respectfully submitted,

Frank S. DiGiglio Registration No. 31,346

SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza Garden City, New York 11530 (516) 742-4343 FSD/XZ:ab

Enclosures:

- Marked-up version of the Sequence Listing;
- Statement Under 37 C.F.R. §1.821(f);
- Copy of the Notice to Comply.

PCT/AU98/00764
RECEIVED



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: (US ONLY): S. CORY, J.A. ADAMS, C. PRINT, L. GIBSON (OTHER THAN US) THE WALTER AND ELIZA HALL INSTITUTE

OF MEDICAL RESEARCH

(ii) TITLE OF INVENTION:

A METHOD OF TREATMENT AND AN ANIMAL

MODEL USEFUL FOR SAME

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE

(B) STREET: 1 LITTLE COLLINS STREET

(C) CITY: MELBOURNE

(D) STATE: VICTORIA

(E) COUNTRY: AUSTRALIA

(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: Patentin Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL

(B) FILING DATE: 16-SEP-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO9228

(B) FILING DATE: 16-SEP-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES, DR E JOHN L

(C) REFERENCE/DOCKET NUMBER: EJH/EK

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777

(B) TELEFAX: +61 3 9254 2770

(C) TELEX: AA 31787

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: [38] base pairs 58 |

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

AAG TG Lys

(A) NAME/KEY: CDS (B) LOCATION: 1. 582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG Met 1	GCG Ala	ACC Thr	CCA Pro	GCC Ala 5	TCG Ser	GCC Ala	CCA Pro	GAC Asp	ACA Thr 10	CGG Arg	GCT Ala	CTG Leu	GTG Val	GCA Ala 15	GAC Asp	48
TTT Phe	GTA Val	GGT Gly	TAT Tyr 20	AAG Lys	CTG Leu	AGG Arg	CAG Gln	AAG Lys 25	GGT	TAT Tyr	GTC Val	TGT Cys	GGA Gly 30	GCT Ala	GGC	96
CCC Pro	GGG Gly	GAG Glu 35	GGC	CCA Pro	GCA Ala	GCT Ala	GAC Asp 40	CCG	CTG Leu	CAC His	CAA Gln	GCC Ala 45	ATG Met	CGG Arg	GCA Ala	144
GCT Ala	GGA Gly 50	GAT Asp	GAG Glu	TTC Phe	GAG Glu	ACC Thr 55	CGC Arg	TTC Phe	CGG Arg	CGC Arg	ACC Thr 60	TTC Phe	TCT	GAT Asp	CTG Leu	192
GCG Ala 65	GCT Ala	CAG Gln	CTG Leu	CAT His	GTG Val 70	ACC Thr	CCA Pro	GGC	TCA Ser	GCC Ala 75	CAA Gln	CAA Gln	CGC Arg	TTC Phe	ACC Thr 80	240
CAG Gln	GTC Val	TCC Ser	GAT Asp	GAA Glu 85	CTT Leu	TTT	CAA Gln	GGG Gly	GGC Gly 90	Pro	AAC Asn	TGG Trp	GGC Gly	CGC Arg 95	CTT Leu	288
GTA Val	GCC Ala	TTC Phe	TTT Phe 100	GTC Val	TTT Phe	GGG Gly	GCT Ala	GCA Ala 105	CTG Leu	TGT Cys	GCT Ala	GAG Glu	AGT Ser 110	GTC Val	AAC Asn	- 336
ÀAG Lys	GAG Glu	ATG Met 115	GAA Glu	CCA Pro	CTG Leu	GTG Val	GGA Gly 120	CAA Gln	GTG Val	CAG Gln	GAG Glu	TGG Trp 125	ATG Met	GTG Val	GCC Ala	384
TAC Tyr	CTG Leu 130	GAG Glu	ACG Thr	CGG Arg	CTG Leu	GCT Ala 135	GAC Asp	TGG Trp	ATC Ile	CAC His	AGC Ser 140	Ser	GGG Gly	GGC	TGG	432
GCG Ala 145	Glu	TTC Phe	ACA Thi	GCT Ala	CTA Leu 150	Tyr	G17 GGG	GAC	Gly	GCC Ala 155	Leu	GAG Glu	GAG Glu	GCG	CGG Arg 160	480
CGT Arg	CTG Leu	CGG Arg	GAG Glu	GGG Gly 165	Asn	TGG	GCA Ala	TCA Ser	GTG Val 170	Arg	ACA Thr	GTG Val	CTG Leu	ACG Thr 175	GGG Gly	526
GCC Ala	GTG Val	GCA Ala	CTG Leu 180	Gly	GCC Ala	CTG Leu	GTA Val	ACT Thr 185	· Val	GGG	GCC Ala	TTI Phe	TTT Phe 190	ATS	AGC Ser	576.

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
- Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly 20 25 30
- Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala 35 40 45
- Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
- Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr 65 70 75 80
- Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
- Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
- Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
- Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
- Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
- Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
- Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser

									•									
(2)	INF	ORMA	TION	FOR	SEQ	ID I	NO : 3	ا م		,								
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (582 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear																	
•	(ii)	MO1	LECU	LE TY	(PE:	DNA												
	(ix)	FE) (2 (1		E: AME/I OCATI	CEY:	CDS	82)	5	79				,					
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO.3: TG GCG ACC CCA GCC TCA ACC CCA GAC ACA CGG GCT CTA GTG GCT GAC 49																	
ATG Met 1	GCG λla	ACC Thr	CCA Pro	GCC Ala 5	TCA Ser	ACC Thr	CCA Pro	GAC Asp	ACA Thr 10	Yra CGG	GCT Ala	CTA Leu	GTG Val	GCT Ala 15	GAC Asp		49	
rrr Phe	GTA Val	GGC Gly	TAT Tyr 20	AAG Lys	CTG Leu	AGG Arg	CAG Gln	AAG Lys 25	GGT Gly	TAT	GTC Val	TGT Cys	GGA Gly 30	GCT Ala	GIY		96	
CT Pro	GJA GGG	GAA Glu 35	GGC Gly	CCA Pro	GCC Ala	GCC Ala	GAC Asp 40	CCG Pro	CTG Leu	CAC His	CAA Gln	GCC Ala 45	ATG Met	CGG Arg	GCT Ala		144	
GCT Ala	GGA Gly 50	GAC Asp	GAG Glu	TTT Phe	GAG Glu	ACC Thr 55	CGT Arg	TTC Phe	CGC Arg	Arģ CGC	ACC Thr 60	TTC Phe	TCT Ser	GAC Asp	CTG Leu		192	
SCC Ala 65	GCT Ala	CAG Gln	CTA Leu	CAC His	GTG Val 70	ACC Thr	CCA Pro	GGC	TCA Ser	GCC Ala 75	CAG Gln	CAA Gln	CGC Arg	TTC Phe	ACC Thr 80		240	
CAG Gln	GTT Val	TCC Ser	GAC Asp	GAA Glu 85	CTT Leu	TTC Phe	CAA Gln	GGG Gly	GGC Gly GGC	CCT Pro	AAC Asn	TGG Trp	GJA GGC	CGT Arg 95	CTT Leu		288	
STG Val	GCA Ala	TTC Phe	TTT Phe 100	GTC Val	TTT Phe	GGG	GCT Ala	GCC Ala 105	CTG Leu	TGT Cys	GCT Ala	GAG Glu	AGT Ser 110	GTC Val	AAC Asn		336	
AAA Lys	Glu	ATG Met 115	GAG Glu	CCT Pro	Leu	GTG Val	Gly	Gln	GTG Val	Gln	GAT Asp	Trp	Met	GTG Val	GCC Ala		384	· ·
rac Tyr	CTG Leu 130	GAG Glu	ACA Thr	CGT Arg	CTG Leu	GCT Ala 135	GAC Asp	TGG Trp	ATC Ile	CAC His	AGC Ser 140	AGT Ser	GJA GGG	GJY GGC	TGG Trp		432	
GCG Ala 145	GAG Glu	TTC Phe	ACA Thr	GCT Ala	CTA Leu 150	Tyr	GIY GGG	GAC Asp	GGG Gly	GCC Ala 155	CTG Leu	GAG Glu	GAG Glu	GCA Ala	CGG Arg 160		480	
CGT Arg	CTG Leu	CGG Arg	GAG Glu	GGG Gly 165	AAC Asn	TGG Trp	GCA Ala	TCA Ser	GTG Val 170	AGG Arg	ACA Thr	GTG Val	CTG Leu	ACG Thr 175	GCG		528	
GCC Ala	GTG Val	GCA Ala	CTG Leu 180	GGG Gly	GCC Ala	CTG Leu	GTA Val	ACT Thr 185	GTA Val	GCG	GCC	TTT Phe	TTT Phe 190	GCT Ala	AGC Ser		576	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr 65 70 75 80

Gin Val Ser Asp Glu Leu Phe Gin Gly Gly Pro Asn Trp Gly Arg Leu 85 90 95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala 115 120 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser 180 185 190

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTIC5:

(A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

Lys *

(A) NAME/KEY: CDS (B) LOCATION: 1. 583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

		,	_				•									•	
ATG Met 1	GCG Ala	ACC Thr	CCA Pro	GCC Ala 5	TCG Ser	GCC Ala	CCA Pro	GAC Asp	ACA Thr 10	CGG	GCT Ala	CTG Leu	GTG Val	GCA Ala 15	GAC Asp		48
TTT Phe	GTA Val	GGT Gly	TAT Tyr 20	AAG Lys	CTG Leu	AGG Arg	CAG Gln	AAG Lys 25	GGT Gly	TAT Tyr	GTC Val	TGT Cys	GGA Gly 30	GCT Ala	Gly		96
CCC	GGG Gly	GAG Glu 35	GGC	CCA Pro	GCA Ala	GCT Ala	GAC Asp 40	CCG Pro	CTG Leu	CAC His	CAA Gln	GCC Ala 45	ATG Met	CGG Arg	GČA Ala		144
GCT Ala	GGA Gly 50	GAT Asp	GAG Glu	TTC Phe	GAG Glu	ACC Thr 55	CGC	TTC Phe	CGG Arg	CGC	ACC Thr 60	TTC Phe	TCT Ser	GAT Asp	CTG Leu		192
GCG Ala 65	GCT Ala	CAG Gln	CTG Leu	CAT His	GTG Val 70	ACC Thr	CCA Pro	GGC Gly	TCA Ser	GCC Ala 75	CAG Gln	CAA Gln	CGC Arg	TTC Phe	ACC Thr 80	٠	240
CAG Gln	GTC Val	TCC Ser	GAC Asp	GAA Glu 85	CTT Leu	TTT Phe	CAA Gln	GGG	GGC Gly 90	CCC Pro	AAC Asn	TGG Trp	GGC Gly	CGC Arg 95	CTT Leu		288
GTA Val	GCC Ala	TTC Phe	TTT Phe 100	CTC	TTT	GGG	GCT Ala	GCA Ala 105	CTG Leu	TGT Cys	GCT Ala	GAG Glu	AGT Ser 110	GTC Val	AAC Asn		336
AAG Lys	GAG Glu	ATG Met 115	GAA Glu	CCA Pro	CTG Leu	GTG Val	GGA Gly 120	Gln	GTG Val	.CAG Gln	GAG Glu	TGG Trp 125	ATG Met	GTG Val	GCC Ala		384
TAC Tyr	CTG Leu 130	GAG Glu	ACG Thr	CGG Arg	CTG Leu	GTC Val 135	GAC Asp	TGG Trp	ATC	CAC	AGÇ Ser 140	ser	GCG	GGC	TGG		432
GCG Ala 145	Glu	TTC Phe	ACA Thr	GCT Ala	CTA Leu 150	TAC Tyr	GGG	GAC Asp	GGG	GCC Ala 155	Leu	GAG Glu	GAG Glu	GCG Ala	CGG Arg 160		480
CGT	CTG Leu	CGG Arg	GAG Glu	GGG Gly 165	Asn	TGG	GCA Ala	TCA Ser	GTG Val 170	Arg	ACA Thr	GTG Val	CTG Leu	ACG Thr 175	GCG		528
GCC Ala	GTG Val	GCA Ala	CTG Leu 180	GJA	GCC	CTG Leu	GTA Val	ACT Thr 185	Val	GGG Gly	GCC Ala	TTT	TTT Phe 190	ATa	AGC Ser		576
AAG	TGA	A															. 583

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: [194] amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp 10 15

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu 50 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu 85 90 95

Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn 100 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala 115 125

Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp 130 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg 145 150 155

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser 180 185 190

(2)			TION QUEN				33	<u>.</u>							•		
٠	(1	() ()	A) Li B) T C) S D) T	ENGT! YPE : IRAN!	H: (Ŝ nuc DEDN	82]b leic ESS:	ase aci sin	pair. d	s								
•	(11)	MOI	LECUI	LE T	(PE:	DNA		•									
	(ix)) FE () (!	ATURI A) NI B) LO	E: AME/I DCATI	KEY:	CDS	€82 <u>\</u>	5	79		•		•				
	(xi)	SEÇ	QUENC	CE DE	ESCR	[PTIC	ON: 5	SEQ :	ID NO): ₇ :						•	
ATG Met 1	CCG Pro	ACC	CCA Pro	GCC Ala 5	TCA Ser	ACC Thr	CCA Pro	GAC Asp	ACA Thr 10	CGC Arg	GCT Ala	CTA Leu	GTG Val	GCT Ala 15	GAC Asp	٠	48
TTT Phe	GTA Val	GGC Gly	TAT Tyr 20	AGG Arg	CTG Leu	AGG Arg	CAG Gln	AAG Lys 25	GCT	TAT Tyr	GTC Val	TGT Cys	GGA Gly 30	GCT Ala	GGG Gly		96
CCT Pro	Gly GGG	GAA Glu 35	GGC	CCA Pro	GCC Ala	GCC Ala	GAC Asp 40	CCG Pro	Leu	CAC His	CAA Gln	GCC Ala 45	ATG Met	CGG Arg	GCT Ala		.144
GCT Ala	GGA Gly 50	GAC Asp	GAG Glu	TTT Phe	GAG Glu	ACC Thr 55	CGT Arg	TTC Phe	CGC	CGC Arg	ACC Thr 60	TTC Phe	TCT Ser	GAC Asp	CTG Leu		192
GCC Ala 65	GCT Ala	CAG Gln	CTA Leu	CAC His	GTG Val 70	ACC Thr	CCA Pro	GGC Gly	TCA Ser	GCC Ala 75	CAG Gln	CAA Gln	CGC Arg	TTC Phe	ACC Thr 80		240
CAG Gln	GTT Val	TCC Ser	GAC Asp	GAA Glu 85	CTT Leu	TTC Phe	CAA Gln	GJĀ GGG	GGC Gly 90	CCT Pro	AAC Asn	TGG Trp	GGC	CGT Arg .95	CTT Leu		288
GTG Val	GCA Ala	TTC Phe	TTT Phe 100	GTC Val	TTT Phe	GGG	GCT Ala	GCC Ala 105	CTG Leu	TGT Cys	GCT Ala	GAG Glu	AGT Ser 110	GTC Val	AAC Asn	•	336
AAA Lys	GAA Glu	ATG Met 115	GAG Glu	Pro Pro	TTC Leu	GTG Val	GGA Gly 120	CAA Gln	GTC Val	CAG Gln	GAT Asp	TGG Trp 125	ATC Ile	GTG Val	GCC Ala	. ,	384
TAC Tyr	CTG Leu 130	Glu	ACA Thr	CGT	CTG Leu	GCT Ala 135	GAC Asp	TGG Trp	ATC Ile	CAC His	AGC Ser 140	AGT Ser	GGC	GGC	TGG Trp		43,2
GCG Ala 145	GAC Asp	TTC Phe	ACA Thr	Ala	CTA Leu 150	ТАС Туг	GGG	GAC Asp	Gly	GCC Ala 155	CTG Leu	GAG Glu	GAC Asp	GCA Ala	CGG Arg 160		480
CGT Arg	CTG Leu	CGG Arg	GAG Glu	GGC Gly 165	AAC Asn	TGG Trp	Ala	(TGÀ]GTG	Ser	ACA Thr	GTG Val	GTG Val	ACG Thr 175	GIY		52

GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser 180

582 581

AAG TG Lys

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
1 10 15

Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu 85 90 95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala 115 120 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
130 135 140

Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly 165

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser 180 185 190